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OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/783,931

DATE: 12/05/2001  
 TIME: 11:51:31

Input Set : A:\7326-122  
 Output Set: N:\CRF3\11212001\I783931.raw

**ENTERED**

## SEQUENCE LISTING

## C--&gt; 5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Ish-Horowicz, David  
 8 Henrique, Domingos Manuel Pinto  
 9 Lewis, Julian Hart  
 10 Artavanis-Tsakonas, Spyridon  
 11 Gray, Grace

C--> 13 (ii) TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
AND FRAGMENTS

14 (iii) NUMBER OF SEQUENCES: 94

16 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Pennie & Edmonds LLP  
 19 (B) STREET: 1155 Avenue of the Americas  
 20 (C) CITY: New York  
 21 (D) STATE: NY  
 22 (E) COUNTRY: USA  
 23 (F) ZIP: 10036/2711

24 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Diskette  
 27 (B) COMPUTER: IBM Compatible  
 28 (C) OPERATING SYSTEM: DOS  
 29 (D) SOFTWARE: FastSEQ Version 2.0

30 (vi) CURRENT APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/09/783,931  
 C--> 33 (B) FILING DATE: 15-Feb-2001  
 C--> 34 (C) CLASSIFICATION:

40 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/981,392  
 38 (B) FILING DATE: 22-DEC-1997

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Antler, Adriane M.  
 44 (B) REGISTRATION NUMBER: 32,605  
 45 (C) REFERENCE/DOCKET NUMBER: 7326-122

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 212-790-9090  
 49 (B) TELEFAX: 212-869-8864  
 50 (C) TELEX: 66141 PENNIE

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 2508 base pairs  
 57 (B) TYPE: nucleic acid  
 58 (C) STRANDEDNESS: single  
 59 (D) TOPOLOGY: linear

W--&gt; 61 (ii) MOLECULE TYPE: DNA

62 (ix) FEATURE:

64 (A) NAME/KEY: Coding Sequence  
 65 (B) LOCATION: 277...2460

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## (D) OTHER INFORMATION:

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66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69      GAATTCGGCA CGAGTTTTTT TTTTTTTTTT TCCCCCTCTT TTCTTTCTTT TCCTTTTGCC      60
71      ATCCGAAAGA GCTGTCAGCC GCCGCCGGGC TGCACCTAAA GGCCTCGGTA GGGGGATAAC      120
72      AGTCAGAGAC CCTCCTGAAA GCAGGAGACG GGACGGTACC CCTCCGGCTC TGCGGGGCGG      180
73      CTGCGGCCCC TCCGTTCTTT CCCCCTCCCC GAGAGACACT CTCCTTTTCC CCCCACGAAG      240
74      ACACAGGGGC AGGAACGCGA GCGCTGCCCC TCCGCC ATG GGA GGC CGC TTC CTG      294
75      Met Gly Gly Arg Phe Leu
76      1 5
77      CTG ACG CTC GCC CTC CTC TCG GCG CTG CTG TGC CGC TGC CAG GTT GAC      342
79      Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu Cys Arg Cys Gln Val Asp
80      10 20
81      GGC TCC GGG GTG TTC GAG CTG AAG CTG CAG GAG TTT GTC AAC AAG AAG      390
83      Gly Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys
84      25 30 35
85      GGG CTG CTC AGC AAC CGC AAC TGC TGC CGG GGG GGC GGC CCC GGA GGC      438
87      Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg Gly Gly Gly Pro Gly Gly
88      40 45 50
89      GCC GGG CAG CAG CAG TGC GAC TGC AAG ACC TTC TTC CGC GTC TGC CTG      486
91      Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr Phe Phe Arg Val Cys Leu
92      55 60 65 70
93      AAG CAC TAC CAG GCC AGC GTC TCC CCC GAG CCG CCC TGC ACC TAC GGC      534
95      Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
96      75 80 85
97      AGC GCC ATC ACC CCC GTC CTC GGC GCC AAC TCC TTC AGC GTC CCC GAC      582
99      Ser Ala Ile Thr Pro Val Leu Gly Ala Asn Ser Phe Ser Val Pro Asp
100      90 95 100
101      GGC GCG GGC GGC GGC GAC CCC GCC TTC AGC AAC CCC ATC CGC TTC CCC      630
103      Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro
104      105 110 115
105      TTC GGC TTC ACC TGG CCC GGC ACC TTC TCG CTC ATC ATC GAG GCT CTG      678
107      Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu
108      120 125 130
109      CAC ACC GAC TCC CCC GAC GAC CTC ACC ACA GAA AAC CCC GAG CGC CTC      726
111      His Thr Asp Ser Pro Asp Asp Leu Thr Thr Glu Asn Pro Glu Arg Leu
112      135 140 145 150
113      ATC AGC CGC CTG GCC ACC CAG AGG CAC CTG GCG GTG GGC GAG GAG TGG      774
115      Ile Ser Arg Leu Ala Thr Gln Arg His Leu Ala Val Gly Glu Glu Trp
116      155 160 165
117      TCC CAG GAC CTG CAC AGC AGC GGC CGC ACC GAC CTC AAG TAC TCC TAT      822
119      Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr
120      170 175 180
121      CGC TTT GTG TGT GAT GAG CAC TAC TAC GGG GAA GGC TGC TCT GTC TTC      870
123      Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe
124      185 190 195
125      TGC CGG CCC CGT GAC GAC CGC TTC GGT CAC TTC ACC TGT GGA GAG CGT      918
127      Cys Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg
128      200 205 210
129      GGC GAG AAG GTC TGC AAC CCA GGC TGG AAG GGC CAG TAC TGC ACT GAG      966
131

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 132 | Gly | Glu | Lys | Val | Cys | Asn | Pro | Gly | Trp | Lys | Gly | Gln | Tyr | Cys | Thr | Glu |      |
| 133 | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |      |
| 135 | CCG | ATT | TGC | TTG | CCT | GGG | TGT | GAC | GAG | CAG | CAC | GGC | TTC | TGC | GAC | AAA | 1014 |
| 136 | Pro | Ile | Cys | Leu | Pro | Gly | Cys | Asp | Glu | Gln | His | Gly | Phe | Cys | Asp | Lys |      |
| 137 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     |     | 245 |      |
| 139 | CCT | GGG | GAA | TGC | AAG | TGC | AGA | GTG | GGT | TGG | CAG | GGG | CGG | TAC | TGT | GAC | 1062 |
| 140 | Pro | Gly | Glu | Cys | Lys | Cys | Arg | Val | Gly | Trp | Gln | Gly | Arg | Tyr | Cys | Asp |      |
| 141 |     |     |     |     | 250 |     |     |     | 255 |     |     |     |     |     |     | 260 |      |
| 143 | GAG | TGC | ATC | CGA | TAC | CCA | GGC | TGC | CTG | CAC | GGT | ACC | TGT | CAG | CAG | CCA | 1110 |
| 144 | Glu | Cys | Ile | Arg | Tyr | Pro | Gly | Cys | Leu | His | Gly | Thr | Cys | Gln | Gln | Pro |      |
| 145 |     |     |     |     | 265 |     |     |     | 270 |     |     |     |     |     |     | 275 |      |
| 147 | TGG | CAG | TGC | AAC | TGC | CAG | GAA | GGC | TGG | GGC | GGC | CTT | TTC | TGC | AAC | CAG | 1158 |
| 148 | Trp | Gln | Cys | Asn | Cys | Gln | Glu | Gly | Trp | Gly | Gly | Leu | Phe | Cys | Asn | Gln |      |
| 149 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |     |     | 290 |      |
| 151 | GAC | CTG | AAC | TAC | TGC | ACT | CAC | CAC | AAG | CCA | TGC | AAG | AAT | GGT | GCC | ACA | 1206 |
| 152 | Asp | Leu | Asn | Tyr | Cys | Thr | His | His | Lys | Pro | Cys | Lys | Asn | Gly | Ala | Thr |      |
| 153 |     |     |     |     |     | 300 |     |     |     |     |     | 305 |     |     |     | 310 |      |
| 155 | TGC | ACC | AAC | ACC | GGT | CAG | GGG | AGC | TAC | ACT | TGT | TCT | TGC | CGA | CCT | GGG | 1254 |
| 156 | Cys | Thr | Asn | Thr | Gly | Gln | Gly | Ser | Tyr | Thr | Cys | Ser | Cys | Arg | Pro | Gly |      |
| 157 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |     |     |     | 325 |      |
| 159 | TAC | ACA | GGC | TCC | AGC | TGC | GAG | ATT | GAA | ATC | AAC | GAA | TGT | GAT | GCC | AAC | 1302 |
| 160 | Tyr | Thr | Gly | Ser | Ser | Cys | Glu | Ile | Glu | Ile | Asn | Glu | Cys | Asp | Ala | Asn |      |
| 161 |     |     |     |     | 330 |     |     |     | 335 |     |     |     |     |     |     | 340 |      |
| 163 | CCT | TGC | AAG | AAT | GGT | GGA | AGC | TGC | ACG | GAT | CTC | GAG | AAC | AGC | TAT | TCC | 1350 |
| 164 | Pro | Cys | Lys | Asn | Gly | Gly | Ser | Cys | Thr | Asp | Leu | Glu | Asn | Ser | Tyr | Ser |      |
| 165 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |     |     |     | 355 |      |
| 167 | TGT | ACC | TGC | CCC | CCA | GGC | TTC | TAT | GGT | AAA | AAC | TGT | GAG | CTG | AGT | GCA | 1398 |
| 168 | Cys | Thr | Cys | Pro | Pro | Gly | Phe | Tyr | Gly | Lys | Asn | Cys | Glu | Leu | Ser | Ala |      |
| 169 |     |     |     |     |     | 360 |     |     | 365 |     |     |     |     |     |     | 370 |      |
| 171 | ATG | ACT | TGT | GCT | GAT | GGA | CCG | TGC | TTC | AAT | GGA | GGG | CGA | TGC | ACT | GAC | 1446 |
| 172 | Met | Thr | Cys | Ala | Asp | Gly | Pro | Cys | Phe | Asn | Gly | Gly | Arg | Cys | Thr | Asp |      |
| 173 |     |     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |      |
| 175 | AAC | CCT | GAT | GGT | GGA | TAC | AGC | TGC | CGC | TGC | CCA | CTG | GGT | TAT | TCT | GGG | 1494 |
| 176 | Asn | Pro | Asp | Gly | Gly | Tyr | Ser | Cys | Arg | Cys | Pro | Leu | Gly | Tyr | Ser | Gly |      |
| 177 |     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     |     | 405 |      |
| 179 | TTC | AAC | TGT | GAA | AAG | AAA | ATC | GAT | TAC | TGC | AGT | TCC | AGC | CCT | TGT | GCT | 1542 |
| 180 | Phe | Asn | Cys | Glu | Lys | Lys | Ile | Asp | Tyr | Cys | Ser | Ser | Ser | Pro | Cys | Ala |      |
| 181 |     |     |     |     | 410 |     |     |     | 415 |     |     |     |     |     |     | 420 |      |
| 183 | AAT | GGA | GCC | CAG | TGC | GTT | GAC | CTG | GGG | AAC | TCC | TAC | ATA | TGC | CAG | TGC | 1590 |
| 184 | Asn | Gly | Ala | Gln | Cys | Val | Asp | Leu | Gly | Asn | Ser | Tyr | Ile | Cys | Gln | Cys |      |
| 185 |     |     |     |     | 425 |     |     |     | 430 |     |     |     |     |     |     | 435 |      |
| 187 | CAG | GCT | GGC | TTC | ACT | GGC | AGG | CAC | TGT | GAC | GAC | AAC | GTG | GAC | GAT | TGC | 1638 |
| 188 | Gln | Ala | Gly | Phe | Thr | Gly | Arg | His | Cys | Asp | Asp | Asn | Val | Asp | Asp | Cys |      |
| 189 |     |     |     |     |     | 440 |     |     | 445 |     |     |     |     |     |     | 450 |      |
| 191 | GCC | TCC | TTC | CCC | TGC | GTC | AAT | GGA | GGG | ACC | TGT | CAG | GAT | GGG | GTC | AAC | 1686 |
| 192 | Ala | Ser | Phe | Pro | Cys | Val | Asn | Gly | Gly | Thr | Cys | Gln | Asp | Gly | Val | Asn |      |
| 193 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |      |
| 195 | GAC | TAC | TCC | TGC | ACC | TGC | CCC | CCG | GGA | TAC | AAC | GGG | AAG | AAC | TGC | AGC | 1734 |
| 196 | Asp | Tyr | Ser | Cys | Thr | Cys | Pro | Pro | Gly | Tyr | Asn | Gly | Lys | Asn | Cys | Ser |      |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|------|
| 197 |     |     |     |     | 475 |     |     |     | 480 |     |     |     |     | 485 |     |     |  |      |      |
| 199 | ACG | CCG | GTG | AGC | AGA | TGC | GAG | CAC | AAC | CCC | TGC | CAC | AAT | GGG | GCC | ACC |  |      | 1782 |
| 200 | Thr | Pro | Val | Ser | Arg | Cys | Glu | His | Asn | Pro | Cys | His | Asn | Gly | Ala | Thr |  |      |      |
| 201 |     |     |     |     | 490 |     |     |     | 495 |     |     |     |     | 500 |     |     |  |      |      |
| 203 | TGC | CAC | GAG | AGA | AGC | AAC | CGC | TAC | GTG | TGC | GAG | TGC | GCT | CGG | GGC | TAC |  |      | 1830 |
| 204 | Cys | His | Glu | Arg | Ser | Asn | Arg | Tyr | Val | Cys | Glu | Cys | Ala | Arg | Gly | Tyr |  |      |      |
| 205 |     |     |     |     | 505 |     |     |     | 510 |     |     |     |     | 515 |     |     |  |      |      |
| 207 | GGC | GGC | CTC | AAC | TGC | CAG | TTC | CTG | CTC | CCC | GAG | CCA | CCT | CAG | GGG | CCG |  |      | 1878 |
| 208 | Gly | Gly | Leu | Asn | Cys | Gln | Phe | Leu | Leu | Pro | Glu | Pro | Pro | Gln | Gly | Pro |  |      |      |
| 209 |     |     |     |     | 520 |     |     |     | 525 |     |     |     |     | 530 |     |     |  |      |      |
| 211 | GTC | ATC | GTT | GAC | TTC | ACC | GAG | AAG | TAC | ACA | GAG | GGC | CAG | AAC | AGC | CAG |  |      | 1926 |
| 212 | Val | Ile | Val | Asp | Phe | Thr | Glu | Lys | Tyr | Thr | Glu | Gly | Gln | Asn | Ser | Gln |  |      |      |
| 213 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 215 | TTT | CCC | TGG | ATC | GCA | GTG | TGC | GCC | GGG | ATT | ATT | CTG | GTC | CTC | ATG | CTG |  |      | 1974 |
| 216 | Phe | Pro | Trp | Ile | Ala | Val | Cys | Ala | Gly | Ile | Ile | Leu | Val | Leu | Met | Leu |  |      |      |
| 217 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 219 | CTG | CTG | GGT | TGC | GCC | ATC | GTC | GTC | TGC | GTC | AGG | CTG | AAG | GTG | CAG |     |  | 2022 |      |
| 220 | Leu | Leu | Gly | Cys | Ala | Ala | Ile | Val | Val | Cys | Val | Arg | Leu | Lys | Val | Gln |  |      |      |
| 221 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 223 | AAG | AGG | CAC | CAC | CAG | CCC | GAG | GCC | TGC | AGG | AGT | GAA | ACG | GAG | ACC | ATG |  |      | 2070 |
| 224 | Lys | Arg | His | His | Gln | Pro | Glu | Ala | Cys | Arg | Ser | Glu | Thr | Glu | Thr | Met |  |      |      |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 227 | AAC | AAC | CTG | GCG | AAC | TGC | CAG | CGC | GAG | AAG | GAC | ATC | TCC | ATC | AGC | GTC |  |      | 2118 |
| 228 | Asn | Asn | Leu | Ala | Asn | Cys | Gln | Arg | Glu | Lys | Asp | Ile | Ser | Ile | Ser | Val |  |      |      |
| 229 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 231 | ATC | GGT | GCC | ACT | CAG | ATT | AAA | AAC | ACA | AAT | AAG | AAA | GTA | GAC | TTT | CAC |  |      | 2166 |
| 232 | Ile | Gly | Ala | Thr | Gln | Ile | Lys | Asn | Thr | Asn | Lys | Lys | Val | Asp | Phe | His |  |      |      |
| 233 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 235 | AGC | GAT | AAC | TCC | GAT | AAA | AAC | GGC | TAC | AAA | GTT | AGA | TAC | CCA | TCA | GTG |  |      | 2214 |
| 236 | Ser | Asp | Asn | Ser | Asp | Lys | Asn | Gly | Tyr | Lys | Val | Arg | Tyr | Pro | Ser | Val |  |      |      |
| 237 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 239 | GAT | TAC | AAT | TTG | GTG | CAT | GAA | CTC | AAG | AAT | GAG | GAC | TCT | GTG | AAA | GAG |  |      | 2262 |
| 240 | Asp | Tyr | Asn | Leu | Val | His | Glu | Leu | Lys | Asn | Glu | Asp | Ser | Val | Lys | Glu |  |      |      |
| 241 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |
| 243 | GAG | CAT | GGC | AAA | TGC | GAA | GCC | AAG | TGT | GAA | ACG | TAT | GAT | TCA | GAG | GCA |  |      | 2310 |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |      |

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266      (i) SEQUENCE CHARACTERISTICS:
267          (A) LENGTH: 728 amino acids
268          (B) TYPE: amino acid
269          (C) STRANDEDNESS:
270          (D) TOPOLOGY: unknown
272      (ii) MOLECULE TYPE: protein
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
276 Met Gly Gly Arg Phe Leu Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu
277   1      5      10      15
278 Cys Arg Cys Gln Val Asp Gly Ser Gly Val Phe Glu Leu Lys Leu Gln
279      20      25      30
280 Glu Phe Val Asn Lys Lys Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg
281      35      40      45
282 Gly Gly Gly Pro Gly Gly Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr
283      50      55      60
284 Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser Pro Glu
285      65      70      75      80
286 Pro Pro Cys Thr Tyr Gly Ser Ala Ile Thr Pro Val Leu Gly Ala Asn
287      85      90      95
288 Ser Phe Ser Val Pro Asp Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser
289      100     105     110
290 Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser
291      115     120     125
292 Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Thr Thr
293      130     135     140
294 Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu
295      145     150     155     160
296 Ala Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr
297      165     170     175
298 Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly
299      180     185     190
300 Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Arg Phe Gly His
301      195     200     205
302 Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys
303      210     215     220
304 Gly Gln Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln
305      225     230     235     240
306 His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp
307      245     250     255
308 Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His
309      260     265     270
310 Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly
311      275     280     285
312 Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro
313      290     295     300
314 Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr
315      305     310     315     320
316 Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile
317      325     330     335

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## VERIFICATION SUMMARY

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Input Set : A:\7326-122

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L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:61 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1  
L:377 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4  
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=14  
L:1201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:1245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1433 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:1510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:1765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42  
L:1891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:1943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45  
L:1964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L:2075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:2094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/783,931

DATE: 12/05/2001  
TIME: 11:51:32

Input Set : A:\7326-122  
Output Set: N:\CRF3\11212001\I783931.raw

L:2096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52  
L:2228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:2251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:2268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:2270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:2295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64  
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64  
L:2611 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=81  
L:2645 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=82  
L:2723 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=86  
L:2762 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87  
L:2807 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89  
L:2852 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91  
L:2897 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93